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 DEFINITION Sequence 255 from Patent WO0208284. DNA linear PAT 06-JUL-2002
 ACCESSION AX454670
 VERSION AX454670.1 GI:21713959
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS
 1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
 Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
 and Ye, W.
 Compositions and methods for the diagnosis and treatment of
 disorders involving angiogenesis
 Patent: WO 0208284-A 255 31-JAN-2002;
 Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone
 (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,
 Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);
 Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US);
 Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US);
 Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
 I. (US)
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 ACCESSION AX491148
 VERSION AX491148.1 GI:22323911
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS
 1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
 Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
 and Ye, W.
 Compositions and methods for the diagnosis and treatment of
 disorders involving angiogenesis


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DEFINITION Sequence 60 from patent US 6627741.
ACCESSION AR404271
VERSION AR404271.1 GI:40152369
KEYWORDS
SOURCE Unknown.
ORGANISM
Unclassified.
REFERENCE
1. (bases 1 to 1161)
Ruben, S.M., Ni, J., Rosen, C.A., Wei, Y.-F., Young, P.E., Florence, K.A.,
Soppet, D.R., Brewer, L.A., Endress, G.A., Carter, K.C., Mucenski, M.,
Ebner, R., LaFleur, D.W., Olsen, H., Shi, Y., Moore, P.A. and
Komatsoulis, G.
TITLE Antibodies to secreted protein HCEJQ69
JOURNAL Patent: US 6627741-A 60 30-SEP-2003;
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Best Local Similarity 99.3%; Pred. No. 2.5e-231;
Matches 1080; Conservative 0; Mismatches 2; Indels 6; Gaps 2;

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LOCUS 94 human secretory proteins.
DEFINITION
ACCESSION BD223456
VERSION BD223456.1 GI:33033226
KEYWORDS JP 2002518010-A/59.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 1161)
Ruben, S.M., Ni, J., Rosen, C.A., Wei, Y.F., Young, P.E., Florence, K.A.,
Soppet, D.R., Brewer, L.A., Endress, G.A., Carter, K.C., Mucenski, M.,
Ebner, R., LaFleur, D.W., Olsen, H.S., Shi, Y., Moore, P.A. and
Komatsoulis, G.
94 human secretory proteins
Patent: JP 2002518010-A 59 25-JUN-2002;
HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002518010-A/59
PD 25-JUN-2002
PF 15-JUN-1998 US 60/089509,16-JUN-1998 US 60/089510 PR
16-JUN-1998 US 60/089508,16-JUN-1998 US 60/089507 PR
22-JUN-1998 US 60/090112,22-JUN-1998 US 60/090113 PI STEVEN
M RUBEN, JIAN NI, CRAIG A ROSEN, YING
PEI WEI, PAUL E YOUNG,
PI KIMBERLY A FLORENCE, DANIEL R SOPPET, LAURIE A BREWER, GREGORY A
PI ENDRESS,
PI KENNETH C CARTER, MICHAEL MUCENSKI, REINHARD EBNER, DAVID W PI
LAFLEUR,
PI HENRIK S OLSEN, YANGGU SHI, PAUL A MOORE, GEORGE KOMATSOUKIS PC

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DEFINITION	Homo sapiens chromosome 3, clone RP11-129K12, complete sequence.		
ACCESSION	AC011816		
VERSION	AC011816.17	GI:11693399	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.		
TITLE	1 (bases 1 to 169313)		
JOURNAL	Homo sapiens chromosome 3, clone RP11-129K12		
REFERENCE	2 (bases 1 to 169313)		
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhealter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donelan,D., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Titrill,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
REFERENCE	3 (bases 1 to 169313)		
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barna,N., Bastien,J., Boguslavsky,L., Boukhealter,B., Brown,A., Canarata,J., Campopiano,A., Chepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Glinde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., Larocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrim,J., Meneus,L., Mihova,I., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rodov,P., Roman,J., Rosetti,M.,		

Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P.,
Souarez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Triggilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission

Submitted (13-FEB-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 13, 2000 this sequence version replaced gi:11181810.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submission@genome.wi.mit.edu

----- Project Information

Center project name: Li841

Center clone name: 129_K_12

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complement(30416. .30590)
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30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tatenos, M., Catanese, J.J. and de Jong, P.J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pister de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-466N21; the clone sequenced to the right is RP11-79N18. Actual start of this clone is at base position 1 of RP11-44N22; actual end is at base position 209161 of RP11-44N22.

FEATURES

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DEFINITION Sequence 267 from Patent WO0129221.
ACCESSION AX119103
VERSION AX119103.1 GI:14036057
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Conklin,D.C. and Yee,D.P.
TITLE Proteins and polynucleotides encoding them
JOURNAL Patent: WO 0129221-A 267 26-APR-2001;
ZymoGenetics, Inc. (US)
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Search completed: June 18, 2004, 03:29:40
Job time : 7052 secs

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3	42.4	3.9	7218	1	US-08-232-463-14	Sequence 14, Appl
4	41	3.7	4713	4	US-09-833-381-897	Sequence 897, App
5	40	3.6	2193	4	US-09-427-261-2	Sequence 2, Appl
6	40	3.6	2193	4	US-09-427-261-3	Sequence 3, Appl
7	39.8	3.6	780	4	US-09-252-991A-5299	Sequence 5299, Ap
8	39.8	3.6	882	4	US-09-252-991A-5334	Sequence 5334, Ap
9	39.8	3.6	1020	4	US-09-489-039A-106	Sequence 106, App
10	39.8	3.6	1968	4	US-09-252-991A-5235	Sequence 5235, Ap
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RESULTS 2
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; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: PZQ291
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12

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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
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; FILING DATE: US/08/232.463
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE: EP 91 114 300.6
; APPLICATION NUMBER: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid

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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PT2gpt-F1s
US-08-232-463-14

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RESULT 4

US-09-833-381-897
; Sequence 897, Application US/09833381
; Patent No. 8672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 897
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-897

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RESULT 5

US-09-427-261-2
; Sequence 2, Application US/09427261A
; Patent No. 6368811
; GENERAL INFORMATION:
; APPLICANT: Grootjans, Jan
; APPLICANT: Zimmerman, Pascale
; APPLICANT: David, Guido
; TITLE OF INVENTION: Syndecan Interacting Proteins and the Use Thereof

RESULT 7
US-09-252-991A-5299
; Sequence 5299, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

RESULT 9
US-09-489-039A-106
; Sequence 106, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND

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QY 566 AGTCAATGTCCAGCAGATCCCC 587

Db 1605 CGAGTCGCCAGCATCAAGCCC 1626

RESULT 12

US-08-471-044-18

; Sequence 18, Application US/08471044

; Patent No. 5840868

; GENERAL INFORMATION:

; APPLICANT: Warren, Gregory W

; APPLICANT: Koziel, Michael G

; APPLICANT: Mullins, Martha A

; APPLICANT: Nye, Gordon J

; APPLICANT: Carr, Brian

; APPLICANT: Dessi, Nalini M

; APPLICANT: Kostichka, N. Kristy

; APPLICANT: Duck, Nicholas B

; APPLICANT: Estruch, Juan J

; TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: NY

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/471,044

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/463,483

; FILING DATE: 05-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/314,594

; FILING DATE: 09-SEP-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/218,018

; FILING DATE: 23-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/037,057

; FILING DATE: 25-MAR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Pace, Gary M.

; REGISTRATION NUMBER: 40,403

; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SQLv3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-541-8582

; TELEFAX: 919-541-8689

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2004 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 1..2004

; OTHER INFORMATION: /note= "Maize optimized DNA

; OTHER INFORMATION: sequence for VIP1A(a) 80 kd protein from AB78"

US-08-471-044-18

Query Match 3.8%; Score 39.6; DB 2; Length 2004;

Best Local Similarity 46.9%; Pred. No. 1.5;

Matches 123; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 326 GGTGGAGAGGGGGGTGCTTCTCTCCCAAGACTCGGTTGGTCCAGGAGCAGCGG 385

Db 1365 GCTGAACAAGAACCGGAGCTACTACATCAGCTGTACATGAGAGGAGAACACCCA 1424

QY 386 GCGGGCGGTGATCATCTCTGCAACACCGAGTTGACATGACAGCTTCTACGTGGAGATGAT 445

Db 1425 GTGGAGATCACCATCGACGGGGAGATATACCCCATCACCACCAAGACCGTGAACGGTAA 1484

QY 446 CCAGGACAGTACCCAGCGCACAGCTGACATCCCGCCCTCTTCTGTGTCGCGCGAGACGG 505

Db 1485 CAAGGACAACCTACAAGCGCTGACATCATGCCCAACAACATCAAGACCAACCCCATCAG 1544

QY 506 CTACATGATCGGCGGTCTCTGGAACAGCATGGGTGCCATGGGCCATCATTTCCATCCC 565

Db 1545 CAGCTGCATCAAGACCAACGACGAGATCACCTGTTCTGGGACGACATATCGATTAC 1604

QY 566 AGTCAATGTCCAGCAGATCCCC 587

Db 1605 CGAGTCGCCAGCATCAAGCCC 1626

RESULT 13

US-08-463-483A-18

; Sequence 18, Application US/08463483A

; Patent No. 5849870

; GENERAL INFORMATION:

; APPLICANT: Warren, Gregory W

; APPLICANT: Koziel, Michael G

; APPLICANT: Mullins, Martha A

; APPLICANT: Nye, Gordon J

; APPLICANT: Carr, Brian

; APPLICANT: Dessi, Nalini M

; APPLICANT: Kostichka, N. Kristy

; APPLICANT: Duck, Nicholas B

; APPLICANT: Estruch, Juan J

; TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: NY

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/463,483A

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/314,594

; FILING DATE: 09-SEP-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/218,018

; FILING DATE: 23-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/037,057

; FILING DATE: 25-MAR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Spruill, W. Murray

; REGISTRATION NUMBER: 32,943

; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2004 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2004
OTHER INFORMATION: /note= "Maize optimized DNA
US-08-463-483A-18
Query Match 3.6%; Score 39.6; DB 2; Length 2004;
Best Local Similarity 46.9%; Pred. No. 1.5;
Matches 123; Conservative 0; Mismatches 139; Indels 0; Gaps 0;
QY 326 GTGGAGAGGGGGCTGCTCTCTCCAAAGACTCGGGTGGTCCAGGAGCAGCGGG 385
DB 1365 GCTGAACAAGAACCGCACTACTACATCAGCCTGTATCAAGAGCGAGAACACCCA 1424
QY 386 GCGGGCGGTGATCATCTCTGACAAAGCAGTGTGACATGACAGCTTCTACGTGGAGATGAT 445
DB 1425 GTGCGAGATCACCATCGACGGCGAGATATACCCCATCACCACCAAGACCGTGAACGTGAA 1484
QY 446 CCAGGACAGTACCCAGGCGACAGTGCATCTCCCGGCTCTCTCTGCTCGGGCGAGACGG 505
DB 1485 CAAGGACAACTACAAGCGCTTGACATCATCGCCCAACATCAAGAGCAACCCCATCAG 1544
QY 506 CTACATGATCGCGGCTCTCTGGAACAGCATGGCTGGCCATGGGCCATCATTTTCCATCCC 565
DB 1545 CAGCTGCACATCAAGACCAACAGCAGATCACCCTGTCTTGGAGGACATATCGATTAC 1604
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DB 1605 CGAGTCGCCAGCATCAAGCCC 1626

RESULT 14

US-08-471-046A-18
Sequence 18, Application US/08471046A
Patent No. 5866326
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Kozziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5866326artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,046A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 - SOLV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2004 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2004
OTHER INFORMATION: /note= "Maize optimized DNA
US-08-471-046A-18
Query Match 3.6%; Score 39.6; DB 2; Length 2004;
Best Local Similarity 46.9%; Pred. No. 1.5;
Matches 123; Conservative 0; Mismatches 139; Indels 0; Gaps 0;
QY 326 GTGGAGAGGGGGCTGCTCTCTCCAAAGACTCGGGTGGTCCAGGAGCAGCGGG 385
DB 1365 GCTGAACAAGAACCGCACTACTACATCAGCCTGTATCAAGAGCGAGAACACCCA 1424
QY 386 GCGGGCGGTGATCATCTCTGACAAAGCAGTGTGACATGACAGCTTCTACGTGGAGATGAT 445
DB 1425 GTGCGAGATCACCATCGACGGCGAGATATACCCCATCACCACCAAGACCGTGAACGTGAA 1484
QY 446 CCAGGACAGTACCCAGGCGACAGTGCATCTCCCGGCTCTCTCTGCTCGGGCGAGACGG 505
DB 1485 CAAGGACAACTACAAGCGCTTGACATCATCGCCCAACATCAAGAGCAACCCCATCAG 1544
QY 506 CTACATGATCGCGGCTCTCTGGAACAGCATGGCTGGCCATGGGCCATCATTTTCCATCCC 565
DB 1545 CAGCTGCACATCAAGACCAACAGCAGATCACCCTGTCTTGGAGGACATATCGATTAC 1604
QY 566 AGTCAATGTACAGCATATCCCC 587
DB 1605 CGAGTCGCCAGCATCAAGCCC 1626

RESULT 15

US-08-470-566B-18
Sequence 18, Application US/08470566B
Patent No. 5872212
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Kozziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2004, 22:32:36 ; Search time 683 Seconds
(without alignments)
6829.460 Million cell updates/sec

Title: US-10-017-306A-375
Perfect score: 1098
Sequence: 1 ggcagcgcgcgcgcgccg.....aaaaaaaaaaaaaaaaaaaaa 1098

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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3	1098	100.0	1098	4	RAF5465 DNA enco
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5	1098	100.0	1098	6	ABK3638 cDNA enco
6	1098	100.0	1098	6	ABK3638 Human PRO
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8	1098	100.0	1098	6	ABL9568 Human ang
9	1098	100.0	1098	7	ABX7830 Human PRO
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11	1098	100.0	1098	7	ACA71282 Human sec
12	1098	100.0	1098	7	ACC87810 Human sec
13	1098	100.0	1098	7	ACC87196 Human sec
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20	1098	100.0	1098	7	ACA66943 cDNA enco
21	1098	100.0	1098	7	ACD15478 Human sec
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					ACF15706 Human sec

24	1098	100.0	1098	7	ACD68695 Novel hum
25	1098	100.0	1098	7	ACA73073 Human PRO
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27	1098	100.0	1098	7	ACD02060 Novel hum
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ALIGNMENTS

RESULT 1
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ID AAA99906 standard; cDNA; 1098 BP.
XX AC AAA99906;
XX DT 26-JAN-2001 (first entry)
XX DE cDNA encoding human protein PRO760.
XX KW Cardiovascular; endothelial; angiogenic disorder; PRO179; PRO238; PRO364;
KW PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333; PRO840; PRO877; PRO878;
KW PRO879; PRO882; PRO885; PRO887; gene therapy; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 60..626
XX FT /*tag= a
XX PN WO200053757-A2.
XX PD 14-SEP-2000.
XX PF 24-FEB-2000; 2000WO-US005004.
XX PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028403.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
PI Goddard A, Gurney AL, Hillian KJ, Marsters SA, Pachi NF, Pitti RM;
PI Watanabe CK, Williams PM, Wood WI;

[illegible]

[illegible]

XX	WO200078961-A1.
PN	
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PD	28-DEC-2000.
XX	
PP	18-FEB-2000; 2000WO-US004342.
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PP	23-JUN-1999; 99US-0141037P.
PR	20-JUL-1999; 99US-0144758P.
PR	26-JUL-1999; 99US-0145698P.
PR	01-SEP-1999; 99WO-US020111.
PR	29-OCT-1999; 99US-0162506P.
PR	30-NOV-1999; 99WO-US028313.
PR	02-DEC-1999; 99WO-US028551.
PR	16-DEC-1999; 99WO-US030095.
PR	05-JAN-2000; 2000WO-US000219.
PR	06-JAN-2000; 2000WO-US000376.
XX	(GETH) GENENTECH INC.
PA	
PI	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI	Gao W, Goddard A, Gołowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI	Pan J, Padani NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI	Williams PM, Wood WI;
XX	
XX	WPI; 2001-071395/08.
DR	
XX	
PT	Secreted and transmembrane proteins and nucleic acids designated PRO,
PT	useful as hybridization probes, in chromosome and gene mapping and gene
PT	therapy.
PS	
PS	Claim 2; Fig 215; 787pp; English.
XX	
CC	The present invention relates to secreted and transmembrane proteins.
CC	These proteins and the DNA encoding them may be used as hybridization
CC	probes, in chromosome and gene mapping and in the generation of anti-
CC	sense RNA and DNA. They may also be used to generate either
CC	transgenic animals or knockout animals which are in turn useful for
CC	development and screening of therapeutically useful reagents. The nucleic
CC	acids may also be used in gene therapy
XX	
XX	Sequence 1098 BP; 249 A; 313 C; 311 G; 225 T; 0 U; 0 Other;
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Query Match 100.0%; Score 1098; DB 4; Length 1098;	
Best Local Similarity 100.0%; Pred. No. 4.2e-262;	
Matches 1098; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db 421 ATGACAGCTTCTAGTGGAGATGATCAGGACAGTACCCAGGCGCACAGCTGACATCCCCG 480
Qy 481 CCTCTCTCTGCTCGGCGGAGAGCGGTACATGATCGCGCGTCTCTGGAACAGCATGGGC 540
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Qy 541 TGCCATGGGCGCATCTTTCATCCAGTCAATGTACACAGCATCCCGACCTTTGAGCTGC 600
Db 541 TGCCATGGGCGCATCTTTCATCCAGTCAATGTACACAGCATCCCGACCTTTGAGCTGC 600
Qy 601 TGCAACGGCGCTGGACCTTCTGTGTAGAGAGTTGTCCACATTCAGGCATAAGTGACT 660
Db 601 TGCAACGGCGCTGGACCTTCTGTGTAGAGAGTTGTCCACATTCAGGCATAAGTGACT 660
Qy 661 CTGAGCTGGAGGGGAAACCCAGGAAATTTGCTACTTGGAAATTTGGAGATAGCATCTGG 720
Db 661 CTGAGCTGGAGGGGAAACCCAGGAAATTTGCTACTTGGAAATTTGGAGATAGCATCTGG 720
Qy 721 GGCAAGTGGAGCCAGGTAGAGGAAAGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCC 780
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Qy 841 AAGAGACAGGCCCCCGGCTTCTGCTAGAACCCGAAACAAAGGAGCTGAAGCGCAGTG 900
Db 841 AAGAGACAGGCCCCCGGCTTCTGCTAGAACCCGAAACAAAGGAGCTGAAGCGCAGTG 900
Qy 901 GCGTGAGAGCCATCTGTACCTGTGCACACTACCTGGTCCAGCTCCCTACCCAGGGT 960
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Db 1081 AAAAAAAAAAAAAAAAAA 1098

RESULT 4

AAS46227

ID AAS46227 standard; cDNA; 1098 BP.

AC AAS46227;

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XX

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XX

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XX

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XX

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.

Claim 2; Fig 605; 774pp; English.

Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders

XX


```
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Qy      961  CTCTGCACAGTGACCTTTCACAGCAGTTGTGGAGTGGTTTAAAGAGCTGGTGTGTTGGGGA 1020
Db      961  CTCTGCACAGTGACCTTTCACAGCAGTTGTGGAGTGGTTTAAAGAGCTGGTGTGTTGGGGA 1020
Qy      1021  CTCATATAACCTCTACTGACTTTTGTAGCAATAAGCTTCTCATCAGGTTGCATAAAAAA 1080
Db      1021  CTCATATAACCTCTACTGACTTTTGTAGCAATAAGCTTCTCATCAGGTTGCATAAAAAA 1080
Qy      1081  AAAAAAAAAAAAAAAAAA 1098
Db      1081  AAAAAAAAAAAAAAAAAA 1098

RESULT 8
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ID  ABX78830 standard; cDNA; 1098 bp.
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XX  15-APR-2003 (first entry)
DE  Human PRO polynucleotide #303.
KW  Human; PRO; gene; ss; cytosolic; tumour; cancer; breast; lung; stomach;
KW  liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW  antibody-dependent enzyme mediated prodrug therapy.
XX
XX  Homo sapiens.
XX
XX  US2003027272-A1.
PD
XX  06-FEB-2003.
XX
XX  21-JUN-2002; 2002US-00176492.
XX
XX  18-SEP-1997; 97US-0059263P.
XX  18-SEP-1997; 97US-0059266P.
XX  17-OCT-1997; 97US-0062250P.
XX  21-OCT-1997; 97US-0063486P.
XX  24-OCT-1997; 97US-0063420P.
XX  24-OCT-1997; 97US-0063421P.
XX  28-OCT-1997; 97US-0063540P.
XX  28-OCT-1997; 97US-0063541P.
XX  28-OCT-1997; 97US-0063544P.
XX  28-OCT-1997; 97US-0063564P.
XX  29-OCT-1997; 97US-0063724P.
XX  31-OCT-1997; 97US-0063870P.
XX  31-OCT-1997; 97US-0064103P.
XX  13-NOV-1997; 97US-0065311P.
XX  21-NOV-1997; 97US-0066120P.
XX  24-NOV-1997; 97US-0066466P.
XX  24-NOV-1997; 97US-0066772P.
XX  11-DEC-1997; 97US-0069335P.
XX  12-DEC-1997; 97US-0069425P.
XX  17-DEC-1997; 97US-0069870P.
XX  18-DEC-1997; 97US-0068017P.
XX  10-MAR-1998; 98US-0077450P.
XX  11-MAR-1998; 98US-0077632P.
XX  20-MAR-1998; 98US-0078886P.
XX  20-MAR-1998; 98US-0078939P.
XX  27-MAR-1998; 98US-0079664P.
XX  31-MAR-1998; 98US-0080107P.
XX  31-MAR-1998; 98US-0080194P.
XX  01-APR-1998; 98US-0080327P.
PR      01-APR-1998; 98US-0080333P.
PR      06-APR-1998; 98US-0081049P.
PR      06-APR-1998; 98US-0081070P.
PR      09-APR-1998; 98US-0081195P.
PR      15-APR-1998; 98US-0081838P.
PR      21-APR-1998; 98US-0082568P.
PR      21-APR-1998; 98US-0082569P.
PR      22-APR-1998; 98US-0082704P.
PR      22-APR-1998; 98US-0082797P.
PR      28-APR-1998; 98US-0083322P.
PR      29-APR-1998; 98US-0083495P.
PR      29-APR-1998; 98US-0083496P.
PR      29-APR-1998; 98US-0083499P.
PR      29-APR-1998; 98US-0083552P.
PR      05-MAY-1998; 98US-0084366P.
PR      06-MAY-1998; 98US-0084414P.
PR      07-MAY-1998; 98US-0084639P.
PR      07-MAY-1998; 98US-0084640P.
PR      07-MAY-1998; 98US-0084643P.
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Publication No. US20030073129A1
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I
TITLE OF INVENTION: Secured and Tra
FILE OF INVENTION: Acids Encoding
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/94
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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40	PRIOR FILING DATE: 1998-09-15	40	PRIOR APPLICATION NUMBER: 60/102570
41	PRIOR APPLICATION NUMBER: 60/100584	41	PRIOR FILING DATE: 1998-09-30
42	PRIOR FILING DATE: 1998-09-16	42	PRIOR APPLICATION NUMBER: 60/102571
43	PRIOR APPLICATION NUMBER: 60/100627	43	PRIOR FILING DATE: 1998-09-30
44	PRIOR FILING DATE: 1998-09-16	44	PRIOR APPLICATION NUMBER: 60/102684
45	PRIOR APPLICATION NUMBER: 60/100661	45	PRIOR FILING DATE: 1998-10-01
46	PRIOR FILING DATE: 1998-09-16	46	PRIOR APPLICATION NUMBER: 60/102687
47	PRIOR APPLICATION NUMBER: 60/100662	47	PRIOR FILING DATE: 1998-10-01
48	PRIOR FILING DATE: 1998-09-16	48	PRIOR APPLICATION NUMBER: 60/102965
49	PRIOR APPLICATION NUMBER: 60/100664	49	PRIOR FILING DATE: 1998-10-02
50	PRIOR FILING DATE: 1998-09-16	50	PRIOR APPLICATION NUMBER: 60/103258
51	PRIOR APPLICATION NUMBER: 60/100683	51	PRIOR FILING DATE: 1998-10-06
52	PRIOR FILING DATE: 1998-09-17	52	PRIOR APPLICATION NUMBER: 60/103314
53	PRIOR APPLICATION NUMBER: 60/100684	53	PRIOR FILING DATE: 1998-10-07
54	PRIOR FILING DATE: 1998-09-17	54	PRIOR APPLICATION NUMBER: 60/103315
55	PRIOR APPLICATION NUMBER: 60/100710	55	PRIOR FILING DATE: 1998-10-07
56	PRIOR FILING DATE: 1998-09-17	56	PRIOR APPLICATION NUMBER: 60/103328
57	PRIOR APPLICATION NUMBER: 60/100711	57	PRIOR FILING DATE: 1998-10-07
58	PRIOR FILING DATE: 1998-09-17	58	PRIOR APPLICATION NUMBER: 60/103395
59	PRIOR APPLICATION NUMBER: 60/100848	59	PRIOR FILING DATE: 1998-10-07
60	PRIOR FILING DATE: 1998-09-18	60	PRIOR APPLICATION NUMBER: 60/103396
61	PRIOR APPLICATION NUMBER: 60/100849	61	PRIOR FILING DATE: 1998-10-07
62	PRIOR FILING DATE: 1998-09-18	62	PRIOR APPLICATION NUMBER: 60/103401
63	PRIOR APPLICATION NUMBER: 60/100919	63	PRIOR FILING DATE: 1998-10-07
64	PRIOR FILING DATE: 1998-09-17	64	PRIOR APPLICATION NUMBER: 60/103449
65	PRIOR APPLICATION NUMBER: 60/100930	65	PRIOR FILING DATE: 1998-10-06
66	PRIOR FILING DATE: 1998-09-17	66	PRIOR APPLICATION NUMBER: 60/103633
67	PRIOR APPLICATION NUMBER: 60/101014	67	PRIOR FILING DATE: 1998-10-08
68	PRIOR FILING DATE: 1998-09-18	68	PRIOR APPLICATION NUMBER: 60/103678
69	PRIOR APPLICATION NUMBER: 60/101068	6	

[illegible]

Db	121	CCACGGCTTCGGTATCCAGTAATATTTTGTACTTTCAAGTCTGAGTCCCTGGGGA	CATTC	180	
Qy	181	GATACATCTTTCACAGCCACACTGCTCCAAGGACTTTGGTGTATCTTTTCA	CACAAGGTATG	240	
Db	181	GATACATCTTTCACAGCCACACTGCTCCAAGGACTTTGGTGTATCTTTTCA	CACAAGGTATG	240	
Qy	241	AGCAGATTACCTTGTGCCCGGTGAACCTCCAGAGGCTTCGGGGAACTCAGCA	ACGGTT	300	
Db	241	AGCAGATTACCTTGTGCCCGGTGAACCTCCAGAGGCTTCGGGGAACTCAGCA	ACGGTT	300	
Qy	301	TCTTATCCAGGACCAAGATTGCTCTGTGTGGAGAGGGGGGGTCTCTCTCT	CTCTCCACAAG	360	
Db	301	TCTTATCCAGGACCAAGATTGCTCTGTGTGGAGAGGGGGGGTCTCTCTCT	CTCTCCACAAG	360	
Qy	361	CTCGGTGTTCAGGAGCAGCGCGGGCGGGCGGTGATCTCTGTGACAACGCA	GTGTGACA	420	
Db	361	CTCGGTGTTCAGGAGCAGCGCGGGCGGGCGGTGATCTCTGTGACAACGCA	GTGTGACA	420	
Qy	421	ATCAGACGCTTCTACGTGTGAGATGATCTCAGGACAGTACCAGCGCAGAG	CTGATCCTCCG	480	
Db	421	ATCAGACGCTTCTACGTGTGAGATGATCTCAGGACAGTACCAGCGCAGAG	CTGATCCTCCG	480	
Qy	481	CCCTCTTCCTGTCTCGCGCCGAGACGGCTACATGATCCCGCGCTCTCTG	GAAACAGCATGG	540	
Db	481	CCCTCTTCCTGTCTCGCGCCGAGACGGCTACATGATCCCGCGCTCTCTG	GAAACAGCATGG	540	
Qy	541	TGCCATGGGCCATCATTTCCATCCCGAGTCAATGTACACAGCATCCCACT	TTTGAGCTGTC	600	
Db	541	TGCCATGGGCCATCATTTCCATCCCGAGTCAATGTACACAGCATCCCACT	TTTGAGCTGTC	600	
Qy	601	TGCAACCGCCCTTGGACCTTCTCTGTGTAGAGAGTTTGTCCACATTC	CAGCCATAAGTACT	660	
Db	601	TGCAACCGCCCTTGGACCTTCTCTGTGTAGAGAGTTTGTCCACATTC	CAGCCATAAGTACT	660	
Qy	661	CTGAGCTGGGAAGGGGAAACCCAGGAATTTTGTCTACTTGGAA	TTTGGATAGCATCT	720	
Db	661	CTGAGCTGGGAAGGGGAAACCCAGGAATTTTGTCTACTTGGAA	TTTGGATAGCATCT	720	
Qy	721	GGACAAGTGGAGCCAGGTAGAGGAAAAGGTTTGGCGTTGTAGCTG	TAAAGGGAAGCC	780	
Db	721	GGACAAGTGGAGCCAGGTAGAGGAAAAGGTTTGGCGTTGTAGCTG	TAAAGGGAAGCC	780	
Qy	781	ACACACTGGGCTTCCCTTCCAGGCCCCCAGGGGTGTCTCATGCTAC	AGAAAGAGGC	840	
Db	781	ACACACTGGGCTTCCCTTCCAGGCCCCCAGGGGTGTCTCATGCTAC	AGAAAGAGGC	840	
Qy	841	AAGACAGGCCCCCAGGGCTTCTGGCTAGAACCCGGAACAAAAGAG	CTGAAGCAGGTG	900	
Db	841	AAGACAGGCCCCCAGGGCTTCTGGCTAGAACCCGGAACAAAAGAG	CTGAAGCAGGTG	900	
Qy	901	GCCTGAGAGCCATCTGTGA	CTGTCACTCACTCGGCTCCAGCTCCCTCTACCCAGGTT	960	
Db	901	GCCTGAGAGCCATCTGTGA	CTGTCACTCACTCGGCTCCAGCTCCCTCTACCCAGGTT	960	
Qy	961	CTCTGCACAGTGACCTTCA	CAGCAGTTGTTGGAGTGGTTTAAAGAGCTGTGTG	TGGGGA	1020
Db	961	CTCTGCACAGTGACCTTCA	CAGCAGTTGTTGGAGTGGTTTAAAGAGCTGTGTG	TGGGGA	1020
Qy	1021	CTCAATAAACCCCTCACTGACTTTTTTAGCAATAAGCTTCTCAT	CAGGTTCCCAAAAAA	1080	
Db	1021	CTCAATAAACCCCTCACTGACTTTTTTAGCAATAAGCTTCTCAT	CAGGTTCCCAAAAAA	1080	
Qy	1081	AAAAAAAAAAAAAAAAAA	1098		
Db	1081	AAAAAAAAAAAAAAAAAA	1098		

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1  / APPLICANT: Baker, Kevin P.
2  / APPLICANT: Chen, Jian
3  / APPLICANT: Desnoyers, Luc
4  / APPLICANT: Goddard, Audrey
5  / APPLICANT: Godowski, Paul J.
6  / APPLICANT: Gurney, Austin L.
7  / APPLICANT: Pan, James
8  / APPLICANT: Smith, Victoria
9  / APPLICANT: Watanabe, Colin K.
10 / APPLICANT: Wood, William I.
11 / APPLICANT: Zhang, Zemin
12 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
13 / FILE REFERENCE: P34301C513
14 / CURRENT APPLICATION NUMBER: US/10/206,915
15 / CURRENT FILING DATE: 2002-07-26
16 / PRIOR APPLICATION NUMBER: 10/052586
17 / PRIOR FILING DATE: 2002-01-15
18 / PRIOR APPLICATION NUMBER: 60/059263
19 / PRIOR FILING DATE: 1997-09-18
20 / PRIOR APPLICATION NUMBER: 60/059266
21 / PRIOR FILING DATE: 1997-09-18
22 / PRIOR APPLICATION NUMBER: 60/062250
23 / PRIOR FILING DATE: 1997-10-17
24 / PRIOR APPLICATION NUMBER: 60/063120
25 / PRIOR FILING DATE: 1997-10-24
26 / PRIOR APPLICATION NUMBER: 60/063121
27 / PRIOR FILING DATE: 1997-10-24
28 / PRIOR APPLICATION NUMBER: 60/063486
29 / PRIOR FILING DATE: 1997-10-21
30 / PRIOR APPLICATION NUMBER: 60/063540
31 / PRIOR FILING DATE: 1997-10-28
32 / PRIOR APPLICATION NUMBER: 60/063541
33 / PRIOR FILING DATE: 1997-10-28
34 / PRIOR APPLICATION NUMBER: 60/063544
35 / PRIOR FILING DATE: 1997-10-28
36 / Prior Application data removed - See File Wrapper or PALM.
37 / NUMBER OF SEQ ID NOS: 612
38 / SEQ ID NO 605
39 / LENGTH: 1098
40 / TYPE: DNA
41 / ORGANISM: Homo Sapien
42 / US-10-206-915-605

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Query Match	100.0%; Score 1098; DB 13; Length 1098;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1098; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1	CGGACGCGCGCGGGCGGAGAGAAACCGGCGCGCGCGCGCGCGCGCCCTGGAGA 60
Db	
QY 1	GGGACGCGCGCGGGCGGAGAGAAACCGGCGCGCGCGCGCGCGCCCTGGAGA 60
Db	
QY 61	TGCTCCCCCGCGCGGGCTGCTGTGCTCTGCTGCTCTGCTGCCCGCGTGCCTCGCGG 120
Db	
QY 61	TGCTCCCCCGCGCGGGCTGCTGTGCTCTGCTGCTCTGCTGCCCGCGTGCCTCGCGG 120
Db	
QY 121	CCGACGGTTCGGTATCCATGATATTTGTACTTCAAGTGTGAGTCTGGGACATTC 180
Db	
QY 121	CCGACGGTTCGGTATCCATGATATTTGTACTTCAAGTGTGAGTCTGGGACATTC 180
Db	
QY 181	GATACATCTTCACAGCCACACCTGCCAAGGACTTTGTGGTATCTTTCACACAGAGTATG 240
Db	
QY 181	GATACATCTTCACAGCCACACCTGCCAAGGACTTTGTGGTATCTTTCACACAGAGTATG 240
Db	
QY 241	AGCAGATTCACTTGTCCCGTGGAACTCCAGAGGCTTCGGGGAACTCAGCAACGGTT 300
Db	
QY 241	AGCAGATTCACTTGTCCCGTGGAACTCCAGAGGCTTCGGGGAACTCAGCAACGGTT 300
Db	
QY 301	TCTTTCATCCAGGACCAAGATTGCTGGTGGAGAGGGGGGCTGCTCTTCTCTCCAAAGA 360
Db	
QY 301	TCTTTCATCCAGGACCAAGATTGCTGGTGGAGAGGGGGGCTGCTCTTCTCTCCAAAGA 360
Db	
QY 361	CTCGGCTGGTCCAGGACGACGGCGGGCGGGCTGATCATCTCTCACAAACGAGTTGACA 420
Db	

[illegible]

RESULT 5

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RESULT 5
US-10-201-858-605
; Sequence 605, Application US/10201858
; Publication No. US2004003837A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P343061C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIORITY APPLICATION NUMBER: 10/052586
; PRIORITY FILING DATE: 2002-01-15
; PRIORITY APPLICATION NUMBER: 60/059263
; PRIORITY FILING DATE: 1997-09-18
; PRIORITY APPLICATION NUMBER: 60/059266
; PRIORITY FILING DATE: 1997-09-18
; PRIORITY APPLICATION NUMBER: 60/062250
; PRIORITY FILING DATE: 1997-10-17
; PRIORITY APPLICATION NUMBER: 60/063120
; PRIORITY FILING DATE: 1997-10-24
; PRIORITY APPLICATION NUMBER: 60/063121
; PRIORITY FILING DATE: 1997-10-24
; PRIORITY APPLICATION NUMBER: 60/063486
; PRIORITY FILING DATE: 1997-10-21
; PRIORITY APPLICATION NUMBER: 60/063540
; PRIORITY FILING DATE: 1997-10-28

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; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 605
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-858-605

Query Match          100.0%; Score 1098; DB 13; Length 1098;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1098; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGACGCGCGGGCGGCGAGAGGAAAACGCGCGCGGGCCGGGCCCGGCCTTGAGA 60
Db 1 GCGACGCGCGGGCGGCGAGAGGAAAACGCGCGCGGGCCGGGCCCGGCCTTGAGA 60

Qy 61 TGGTCCCCGGCGCGGGGTGGTTGTCTCTGTGCTCTTGTGCTCCCCTGTGTCGG 120
Db 61 TGGTCCCCGGCGCGGGGTGGTTGTCTCTGTGCTCTTGTGCTCCCCTGTGTCGG 120

Qy 121 CCCACGGCTCCGTATCATGATTATTGTACTTTCAAGTCTGTAGTCTTGGGACATTC 180
Db 121 CCCAGGCTCCGTATCATGATTATTGTACTTTCAAGTCTGTAGTCTTGGGACATTC 180

Qy 181 GATAATCTTCAAGCACACACCTGCCAAGCACTTTGGTGGTATCTTTTCACACAAGGTATG 240
Db 181 GATAATCTTTCACAGCACAACCTGCCAAGCACTTTGGTGGTATCTTTTCACACAAGGTATG 240

Qy 241 AGCAGATTCACTTGTCCCGCTGAACCTCCAGAGGCTCTCGGGGAACTCAGCAAAGGTT 300
Db 241 AGCAGATTCACTTGTCCCGCTGAACCTCCAGAGGCTCTCGGGGAACTCAGCAAAGGTT 300

Qy 301 TCCTTCATCCAGGACCAGATTGCTCTGTGTGAGAGGGGGGCTGCTCTTCTCTCCAAGA 360
Db 301 TCCTTCATCCAGGACCAGATTGCTCTGTGTGAGAGGGGGGCTGCTCTTCTCTCCAAGA 360

Qy 361 CTGGGTGTTCCAGGACACGCGGGCGGGCGGTGATCATCTCTGACACGCAAGTTGACA 420
Db 361 CTGGGTGTTCCAGGACACGCGGGCGGGCGGTGATCATCTCTGACACGCAAGTTGACA 420

Qy 421 ATCAGAGCTTCTACGTGGAGATCATCAGGACAGTAGTACCAGCGCACAGCTGACATCCCG 480
Db 421 ATCAGAGCTTCTACGTGGAGATCATCAGGACAGTAGTACCAGCGCACAGCTGACATCCCG 480

Qy 481 CCCTTTCCTGTCTGGCGGAGACGGCTACATGATCCGCGCTCTCTGGAACAGCATGGGC 540
Db 481 CCCTTTCCTGTCTGGCGGAGACGGCTACATGATCCGCGCTCTCTGGAACAGCATGGGC 540

Qy 541 TGCCATGGGCGCATATTTCCATCCCACTCAATGTCAACAGCATCCCACTTTTGACTGC 600
Db 541 TGCCATGGGCGCATATTTCCATCCCACTCAATGTCAACAGCATCCCACTTTTGACTGC 600

Qy 601 TGCAACGCGCCTGGACCTTCTGTAGAGAGTTGTGCCACATTCAGCCATAAGTGACT 660
Db 601 TGCAACGCGCCTGGACCTTCTGTAGAGAGTTGTGCCACATTCAGCCATAAGTGACT 660

Qy 661 CTGAGCTGGAGGGGAAACCCAGGAATTTTCTGCTACTTTGGANTTTGGAGATGACTG 720
Db 661 CTGAGCTGGAGGGGAAACCCAGGAATTTTCTGCTACTTTGGANTTTGGAGATGACTG 720

Qy 721 GGACAAAGTGGAGCCAGGTAGAGAAAAAGGTTTGGGCGTTGCTAGGCTGAAAGGAAGCC 780
Db 721 GGACAAAGTGGAGCCAGGTAGAGAAAAAGGTTTGGGCGTTGCTAGGCTGAAAGGAAGCC 780

Qy 781 ACACCACTGGCTTCCCTTCCCGAGGCCCCCAAGGGTGTCTCTGCTACAAGAGAGGC 840
Db 781 ACACCACTGGCTTCCCTTCCCGAGGCCCCCAAGGGTGTCTCTGCTACAAGAGAGGC 840

Qy 841 AAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGGAACAAAAGAGAGCTGAAGGACAGTG 900

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DB	181	GATACATCTTTCAAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTTCAACAAGGTATG	241
QY	241	AGCAGATTACCTTGTCTCCCGCTGAACCTTCAGAGGCGCTGCGGGAAGTCTCAGCAACGGTT	300
DB	241	AGCAGATTACCTTGTCTCCCGCTGAACCTTCAGAGGCGCTGCGGGAAGTCTCAGCAACGGTT	300
QY	301	TCCTTATCCAGGACAGATTCTCTGCTGGAGAGGGGGGGTCTCTCTCTCTCCAAAG	360
DB	301	TCCTTATCCAGGACAGATTCTCTGCTGGAGAGGGGGGGTCTCTCTCTCTCCAAAG	360
QY	361	CTCGGTGTGTCCAGGAGCACGCGCGGGCGGGTGATCATCTGTGACAAACGCAAGTTGACA	420
DB	361	CTCGGTGTGTCCAGGAGCACGCGCGGGCGGGTGATCATCTGTGACAAACGCAAGTTGACA	420
QY	421	ATGACAGCTTCTACCTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCG	480
DB	421	ATGACAGCTTCTACCTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCG	480
QY	481	COCTCTTCTGCTCGGCGGAGACGCGCTACATGATCCGCGCTCTCTGGAACAGCATGGGC	540
DB	481	COCTCTTCTGCTCGGCGGAGACGCGCTACATGATCCGCGCTCTCTGGAACAGCATGGGC	540
QY	541	TGCGCATGGGCGCATATTTCCATCCCGATCATGTCACGACATCCCGCATCTTTGAGCTGC	600
DB	541	TGCGCATGGGCGCATATTTCCATCCCGATCATGTCACGACATCCCGCATCTTTGAGCTGC	600
QY	601	TGCAACCGCCCTGGACCTTCTGTGAGAGAGTTTGTCCCATCTTCAGGCATAAGTGACT	660
DB	601	TGCAACCGCCCTGGACCTTCTGTGAGAGAGTTTGTCCCATCTTCAGGCATAAGTGACT	660
QY	661	CTGAGCTGGAGGGGGAACCCAGGATTTTGCTACTTTGGAATTTGGAGATAGCATCTGG	720
DB	661	CTGAGCTGGAGGGGGAACCCAGGATTTTGCTACTTTGGAATTTGGAGATAGCATCTGG	720
QY	721	GGACAAGTGGAGCCAGGTAGAGGAAAAGGTTTGGGCGTTTGTAGGCTCGAAAGGGAAGCC	780
DB	721	GGACAAGTGGAGCCAGGTAGAGGAAAAGGTTTGGGCGTTTGTAGGCTCGAAAGGGAAGCC	780
QY	781	ACACACACTGGCTTCCCTTCCGAGGGCGCCAGGGTGTCTCATGCTACAAGAGAGGC	840
DB	781	ACACACACTGGCTTCCCTTCCGAGGGCGCCAGGGTGTCTCATGCTACAAGAGAGGC	840
QY	841	AAGACACAGGCCCCCAGGGCTTCTGGCTAGAACCCGAAAACAAAGGAGCTTGAAGGCAGGTG	900
DB	841	AAGACACAGGCCCCCAGGGCTTCTGGCTAGAACCCGAAAACAAAGGAGCTTGAAGGCAGGTG	900
QY	901	GCTCAGAGCCATCTGTGACCTGTTCACACTCACCTGGCTCCAGCTCCCGTACCAGGTT	960
DB	901	GCTCAGAGCCATCTGTGACCTGTTCACACTCACCTGGCTCCAGCTCCCGTACCAGGTT	960
QY	961	CTCTGCACAGTGACCTTCACAGCAGTGTGTGGAGTGTTTAAAGAGCTGGTGTTTGGGGA	1020
DB	961	CTCTGCACAGTGACCTTCACAGCAGTGTGTGGAGTGTTTAAAGAGCTGGTGTTTGGGGA	1020
QY	1021	CTCAATTAACCCCTCACTGACTTTTATAGCAATAAGCTTCTCATCAGGGTTGCAAAAAA	1080
DB	1021	CTCAATTAACCCCTCACTGACTTTTATAGCAATAAGCTTCTCATCAGGGTTGCAAAAAA	1080
QY	1081	AAAAAAAAAAAAAAAAAAAA 1098	
DB	1081	AAAAAAAAAAAAAAAAAAAA 1098	

RESULT 7

US-10-219-535-205
; Sequence 205, Application US/10219535
; Publication No. US2004004179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Smith, Victoria
 / APPLICANT: Stephan, Jean-Philippe F.
 / APPLICANT: Watanabe, Colin L.
 / APPLICANT: Wood, William I.
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 / TITLE OF INVENTION: ACIDS ENCODING THE SAME
 / FILE REFERENCE: P3530P1C60
 / CURRENT APPLICATION NUMBER: US/10/219,535
 / CURRENT FILING DATE: 2002-08-14
 / PRIOR APPLICATION NUMBER: 10/119,480
 / PRIOR FILING DATE: 2002-04-09
 / PRIOR APPLICATION NUMBER: 60/059113
 / PRIOR FILING DATE: 1997-09-17
 / PRIOR APPLICATION NUMBER: 60/062287
 / PRIOR FILING DATE: 1997-10-17
 / PRIOR APPLICATION NUMBER: 60/063549
 / PRIOR FILING DATE: 1997-10-28
 / PRIOR APPLICATION NUMBER: 60/064103
 / PRIOR FILING DATE: 1997-10-31
 / PRIOR APPLICATION NUMBER: 60/069873
 / PRIOR FILING DATE: 1997-12-17
 / PRIOR APPLICATION NUMBER: 60/078910
 / PRIOR FILING DATE: 1998-03-20
 / PRIOR APPLICATION NUMBER: 60/079294
 / PRIOR FILING DATE: 1998-03-25
 / PRIOR APPLICATION NUMBER: 60/079656
 / PRIOR FILING DATE: 1998-03-26
 / PRIOR APPLICATION NUMBER: 60/079728
 / PRIOR FILING DATE: 1998-03-27
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 246
 / SEQ ID NO 205
 / LENGTH: 1098
 / TYPE: DNA
 / ORGANISM: Homo Sapien
 / US-10-219-535-205

Query Match	100.0%;	Score 1098;	DB 13;	Length 1098;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1098;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
<hr/>				
QY	1	GGAGCGCGCGGCGGCGAGAGAAACGGCGGCCGGCGCGCGCCCGCCTTGAGA	60	
Dd	1	GGAGCGCGGCGGCGGCGAGAGAAACGGCGGCCGGCGCGCCCGCCTTGAGA	60	
<hr/>				
QY	61	TGGTCCCGGCGCGCGGGGTGGTTGTCGTCTGGCTCCCGCGCTGCCTCGCGG	120	
Dd	61	TGGTCCCGGCGCGCGGGGTGGTTGTCGTCTGGCTCCCGCGCTGCCTCGCGG	120	
<hr/>				
QY	121	CCCAGCGTTCGTATCCATGATATTACTTTCAAGTCTGAGTCTCGGGACAATC	180	
Dd	121	CCCAGCGTTCGTATCCATGATATTACTTTCAAGTCTGAGTCTCGGGACAATC	180	
<hr/>				
QY	181	GATACATCTTCACAGCCACACCTGCCAAGSACTTTGGTGGTATCTTTCACAAAGSTATG	240	
Dd	181	GATACATCTTCACAGCCACACCTGCCAAGSACTTTGGTGGTATCTTTCACAAAGSTATG	240	
<hr/>				
QY	241	AGCAGATTCACTTGTCGCCGCTGAACCTCCAGAGGCTGCGGGAACTCAGCAACGGTT	300	
Dd	241	AGCAGATTCACTTGTCGCCGCTGAACCTCCAGAGGCTGCGGGAACTCAGCAACGGTT	300	
<hr/>				
QY	301	TCTTTCATCCAGGACCAGATTGCTCTGGTGGAGAGGGGGGGTGTCTCTCTCTCCAAGA	360	
Dd	301	TCTTTCATCCAGGACCAGATTGCTCTGGTGGAGAGGGGGGGTGTCTCTCTCTCCAAGA	360	
<hr/>				
QY	361	CTCGGGTGGTTCAGGAGCAGCGCGGGCGGGCGGTGATCATCTCTGACAAACGAGTTGACA	420	
Dd	361	CTCGGGTGGTTCAGGAGCAGCGCGGGCGGGCGGTGATCATCTCTGACAAACGAGTTGACA	420	
<hr/>				
QY	421	ATGACAGCTTCTACGTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCG	480	

;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

;; TITLE OF INVENTION: ACIDS ENCODING THE SAME

;; FILE REFERENCE: P3430RIC41

;; CURRENT APPLICATION NUMBER: US/10/174,581

;; CURRENT FILING DATE: 2002-08-18

;; PRIOR APPLICATION NUMBER: 10/052586

;; PRIOR FILING DATE: 2002-01-15

;; PRIOR APPLICATION NUMBER: 60/059263

;; PRIOR FILING DATE: 1997-09-18

;; PRIOR APPLICATION NUMBER: 60/059266

;; PRIOR FILING DATE: 1997-09-18

;; PRIOR APPLICATION NUMBER: 60/062250

;; PRIOR FILING DATE: 1997-10-17

;; PRIOR APPLICATION NUMBER: 60/063120

;; PRIOR FILING DATE: 1997-10-24

;; PRIOR APPLICATION NUMBER: 60/063121

;; PRIOR FILING DATE: 1997-10-24

;; PRIOR APPLICATION NUMBER: 60/063486

;; PRIOR FILING DATE: 1997-10-21

;; PRIOR APPLICATION NUMBER: 60/063540

;; PRIOR FILING DATE: 1997-10-28

;; PRIOR APPLICATION NUMBER: 60/063541

;; PRIOR FILING DATE: 1997-10-28

;; PRIOR APPLICATION NUMBER: 60/063544

;; PRIOR FILING DATE: 1997-10-28

;; PRIOR APPLICATION NUMBER: 60/063564

;; PRIOR FILING DATE: 1997-10-28

;; PRIOR APPLICATION NUMBER: 60/063734

;; PRIOR FILING DATE: 1997-10-29

;; PRIOR APPLICATION NUMBER: 60/063870

;; PRIOR FILING DATE: 1997-10-31

;; PRIOR APPLICATION NUMBER: 60/064103

;; PRIOR FILING DATE: 1997-10-31

;; PRIOR APPLICATION NUMBER: 60/065311

;; PRIOR FILING DATE: 1997-11-13

;; PRIOR APPLICATION NUMBER: 60/066120

;; PRIOR FILING DATE: 1997-11-21

;; PRIOR APPLICATION NUMBER: 60/066466

;; PRIOR FILING DATE: 1997-11-24

;; PRIOR APPLICATION NUMBER: 60/066772

;; PRIOR FILING DATE: 1997-11-24

;; PRIOR APPLICATION NUMBER: 60/069335

;; PRIOR FILING DATE: 1997-12-11

;; PRIOR APPLICATION NUMBER: 60/069425

;; PRIOR FILING DATE: 1997-12-12

;; PRIOR APPLICATION NUMBER: 60/069870

;; PRIOR FILING DATE: 1997-12-17

;; PRIOR APPLICATION NUMBER: 60/068017

;; PRIOR FILING DATE: 1997-12-18

;; PRIOR APPLICATION NUMBER: 60/077450

;; PRIOR FILING DATE: 1998-03-10

;; PRIOR APPLICATION NUMBER: 60/077632

;; PRIOR FILING DATE: 1998-03-11

;; PRIOR APPLICATION NUMBER: 60/077649

;; PRIOR FILING DATE: 1998-03-11

;; PRIOR APPLICATION NUMBER: 60/078886

;; PRIOR FILING DATE: 1998-03-20

;; PRIOR APPLICATION NUMBER: 60/078939

;; PRIOR FILING DATE: 1998-03-20

;; PRIOR APPLICATION NUMBER: 60/079664

;; PRIOR FILING DATE: 1998-03-27

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;; PRIOR APPLICATION NUMBER: 60/080107

;; PRIOR FILING DATE: 1998-03-31

;; PRIOR APPLICATION NUMBER: 60/080194

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;; PRIOR APPLICATION NUMBER: 60/080327

;; PRIOR FILING DATE: 1998-04-01

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;; PRIOR APPLICATION NUMBER: 60/081195

;; PRIOR FILING DATE: 1998-04-09

;; PRIOR APPLICATION NUMBER: 60/081838

;; PRIOR FILING DATE: 1998-04-15

;; PRIOR APPLICATION NUMBER: 60/082568

;; PRIOR FILING DATE: 1998-04-21

;; PRIOR APPLICATION NUMBER: 60/082569

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;; PRIOR APPLICATION NUMBER: 60/083322

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;; PRIOR FILING DATE: 1998-04-29

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;; PRIOR FILING DATE: 1998-04-29

;; PRIOR APPLICATION NUMBER: 60/083499

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;; PRIOR APPLICATION NUMBER: 60/084414

;; PRIOR FILING DATE: 1998-05-06

;; PRIOR APPLICATION NUMBER: 60/084639

;; PRIOR FILING DATE: 1998-05-07

;; PRIOR APPLICATION NUMBER: 60/084640

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;; PRIOR APPLICATION NUMBER: 60/084643

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;; PRIOR APPLICATION NUMBER: 60/085573

;; PRIOR FILING DATE: 1998-05-15

;; PRIOR APPLICATION NUMBER: 60/085579

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;; PRIOR APPLICATION NUMBER: 60/085580

;; PRIOR FILING DATE: 1998-05-15

;; PRIOR APPLICATION NUMBER: 60/085582

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;; PRIOR APPLICATION NUMBER: 60/085700

;; PRIOR FILING DATE: 1998-05-15

;; PRIOR APPLICATION NUMBER: 60/086023

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;; PRIOR APPLICATION NUMBER: 60/087098

;; PRIOR FILING DATE: 1998-05-28

;; PRIOR APPLICATION NUMBER: 60/087208

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;; PRIOR APPLICATION NUMBER: 60/087609

;; PRIOR FILING DATE: 1998-06-02

;; PRIOR APPLICATION NUMBER: 60/087759

;; PRIOR FILING DATE: 1998-06-02

;; PRIOR APPLICATION NUMBER: 60/087827

;; PRIOR FILING DATE: 1998-06-03

;; PRIOR APPLICATION NUMBER: 60/088025

;; PRIOR FILING DATE: 1998-06-04

;; PRIOR APPLICATION NUMBER: 60/088028

;; PRIOR FILING DATE: 1998-06-04

;; PRIOR APPLICATION NUMBER: 60/088029

;; PRIOR FILING DATE: 1998-06-04

;; PRIOR APPLICATION NUMBER: 60/088033

;; PRIOR FILING DATE: 1998-06-04

;; PRIOR APPLICATION NUMBER: 60/088167

;; PRIOR FILING DATE: 1998-06-05

;; PRIOR APPLICATION NUMBER: 60/088202

;; PRIOR FILING DATE: 1998-06-05

;; PRIOR APPLICATION NUMBER: 60/088212

[illegible]

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Qy 961 CTCTGCACAGTGCACCTTCACACAGTTGTTGGAGTGGTTTAAAGAGCTGGTCTTTGGGGA 1020
Db 961 CTCTGCACAGTGCACCTTCACACAGTTGTTGGAGTGGTTTAAAGAGCTGGTCTTTGGGGA 1020
Qy 1021 CTCATAAAACCCCTCACTGACTTTTTCAGCAATAAAGCTTCTCATCAGGGTTGCAAAAAAA 1080
Db 1021 CTCATAAAACCCCTCACTGACTTTTTCAGCAATAAAGCTTCTCATCAGGGTTGCAAAAAAA 1080
Qy 1081 AAAAAAAAAAAAAAAAAAAAA 1098
Db 1081 AAAAAAAAAAAAAAAAAAAAA 1098

RESULT 14
US-10-176-749-605
; Sequence 605, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RLC76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 605
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-749-605

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QY	61	TGGTCCCCGGCGCGCGGGCTGGTGGT	CTCGTCTCTGGCTCCCGCGTGGCGTCCGGG	120
Db	61	TGGTCCCCGGCGCGCGGGCTGGTGGT	CTCGTCTCTGGCTCCCGCGTGGCGTCCGGG	120
QY	121	CCACGGCTCCGGTATCCATGATTATTTG	TCAATTTCAAGTCTCAGTCTCTGGGGACATTC	180
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QY	181	GATACATCTTCACAGCCACACTGCCAAG	CACTTGGTGGTATCTTTACACAAGGATG	240
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QY	241	AGCAGATTCACTTGTCCCCGTGAACTCC	CAGAGGCTCGCGGGAACTCAGCAACGGTT	300
Db	241	AGCAGATTCACTTGTCCCCGTGAACTCC	CAGAGGCTCGCGGGAACTCAGCAACGGTT	300
QY	301	TCTTCATCCAGGACCAGATTGCTCTG	GTGTGGAGAGGGGGGTGCTCTCTCCAAAG	360
Db	301	TCTTCATCCAGGACCAGATTGCTCTG	GTGTGGAGAGGGGGGTGCTCTCTCCAAAG	360
QY	361	CTCGGGTGTCCAGAGACACGGCGGGCG	GGGTGATCATCTCTGACAAACCGATTGACA	420
Db	361	CTCGGGTGTCCAGAGACACGGCGGGCG	GGGTGATCATCTCTGACAAACCGATTGACA	420

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Qy	481	CCCTCTTCTGCTCGCGCCGAGACGGCTACATGATCCCGCGCTCTCTGGAAACAGCATGGGC	540
Db	481	CCCTCTTCTGCTCGCGCCGAGACGGCTACATGATCCCGCGCTCTCTGGAAACAGCATGGGC	540
Qy	541	TGCCATGGGCCATCATTTCCATCCAGTCATGTGTCACAGCATCCCACTTTGAGCTGC	600
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Db	961	CTCTGCACAGTACCTTTCACAGCAGTTGTTGGAGTGGTTTAAAGAGCTCGTGTTTGGGGA	1020
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Db	1081	AAAAAAAAAAAAAAAAAAAA 1098	

RESULT 15

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US-10-176-914-605
; Sequence 605, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; FILE REFERENCE: P34301C83
; CURRENT APPLICATION NUMBER: US/10/176,914
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612

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Db	961	CTCTGCACAGTGACCTTCACAGCAGTTGTTGGAGTGGTTTAAAGAGCTGGTGTTCGGGA	1020
Qy	1021	CTCAATAAACCCCTCAGTCTTTTGTAGCAATAAAGCTTCTCATCAGGGTTGCAAAAAAA	1080
Db	1021	CTCAATAAACCCCTCAGTCTTTTGTAGCAATAAAGCTTCTCATCAGGGTTGCAAAAAAA	1080
Qy	1081	AAAAAAAAAAAAAAAAAAAA	1098
Db	1081	AAAAAAAAAAAAAAAAAAAA	1098

Search completed: June 18, 2004, 04:59:35
Job time : 717 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2004, 00:56:31 ; Search time 4529 Seconds
(without alignments)
7239.716 Million cell updates/sec

Title: US-10-017-306A-375
Perfect score: 1098
Sequence: 1 ggcacgcggcggggggcgc.....aaaaaaaaaaaaaaaaaa 1098

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2751289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
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13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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17: em_gss_hum:*
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19: em_gss_pln:*
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22: em_gss_mam:*
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26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	887	80.8	949	12	BI765256
2	866.4	78.9	931	13	EX362403
3	860.6	78.4	923	13	EX362402
4	847.4	77.2	898	12	BI262294

5	800.4	72.9	883	13	BUS35678
6	800.2	72.9	867	13	BUS43314
7	780.2	71.1	918	10	BE794928
8	765.4	69.7	1017	12	BM556790
9	750.4	68.3	790	12	BG476497
10	749.4	68.3	901	14	CA489629
11	746.2	68.0	941	10	BE299531
12	724.6	66.0	942	14	CA487422
13	718.2	65.4	813	12	BG789786
14	717	65.3	736	14	CA411866
15	715	65.1	734	12	EM674748
16	713.2	65.0	721	12	EM675323
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18	711.8	64.8	716	14	CA431203
19	706.2	64.3	725	12	BM980396
20	706	64.3	714	14	CB243898
21	705	64.2	774	14	CF453608
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24	693.8	63.2	720	14	CA430357
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30	678.8	61.8	897	13	BQ921550
31	678.4	61.8	694	12	BQ014820
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33	671.6	61.2	733	12	BG770178
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37	645.8	58.8	972	10	BE299584
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40	615.8	56.1	839	13	BQ932162
41	610.2	55.6	642	10	BF000360
42	608.8	55.4	631	10	BE251343
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44	602	54.8	863	12	BI261759
45	598	54.5	631	13	BQ636876

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LOCUS 603050352F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5190564 5', linear EST 25-SEP-2001
DEFINITION mRNA sequence.
ACCESSION BI765256
VERSION BI765256.1 GI:15756834
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hominid
1 (bases 1 to 949)
NIH-MGC Institutes of Health, Mammalian Gene
TITLE National Institutes of Health, Mammalian Gene
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapps@mail.nih.gov
Tissue Procurement: Life Technologies,
CDNA Library Prepared by: The I.M.A.
DNA Sequencing by: Incyte Genomic
Clone distribution: MGC clone d
found through the I.M.A.G.E. Co
http://image.llnl.gov
Plate: LLAM11476 row: 9
High quality sequence stor

Page 2

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 Db CTTTCAAGTCTGAGTCTGGGACATTCGATACATCTTCACAGCCACACCTGCCAAGA 242
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 Db 423 GGTGATCATCTCTGACAAACGAGTTTANCAATGACAGCTTCTACGTGGAGATGATCCAGGA 482
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 QY 572 TGTACACAGATCCCGACCTTTGAGTGTGTGCAACCGCCCTCTCTCTGCTCGGCGGAGAG 631
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 Db 783 TTGGGCGTGTCTAGCTGAAAGGGAAGCCACACCTGCTTCCCTTCCCGAGGGCCCC 842
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 Db 843 CAAGGCTGTCTATGCTACAGAGAGGAGCAGAGCAGCCCGAGGCTTCTGCTAGAA 902
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 Db 903 CCGAAACAAAGAGGCTGAAGCCAGGTG 931

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 LOCUS BX362402 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 DEFINITION Homo sapiens cDNA clone CS0DJ014YP19 3-PRIME, mRNA sequence.
 ACCESSION BX362402
 VERSION BX362402.1 GI:30376617
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 923)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1554.r For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DJ014CH10NP1&cluster=1554.r>. Contact : Feng Liang Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DJ014CH10NP1.

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 /note="1st strand cDNA was primed with a NotI-oligo(GT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Query Match 78.4%; Score 860.6; DB 13; Length 923;
 Best Local Similarity 97.6%; Pred. No. 2.5e-116;
 Matches 869; Conservative 12; Mismatches 8; Indels 1; Gaps 1;
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 QY 792 CTTTCCCTTTCCCGAGGGGGCCCCCAAGGGGTGTCTCTGCTTACAAAGAGGCGCAAGACAGGC 851

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2740 row: o column: 18
High quality sequence stop: 718.

FEATURES
source
1. .883
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6563370"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_107"
/notes="Organ: breast; Vector: pOTB7; Site:1: EcoRI; Site:2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 72.9%; Score 800.4; DB 13; Length 883;
Best Local Similarity 99.8%; Pred. No. 1.6e-107;
Matches 812; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 165 AGTCCTGGGACATTCGATACATCTTCACGCCACACTGCCAAGGACTTTGGTGTATC 224
Db 1 AGTCCTGGGACATTCGATACATCTTCACGCCACACTGCCAAGGACTTTGGTGTATC 60

QY 225 TTTCACACAGTATGACAGATTCACCTTCCCGCTGAACTCCAGAGCCCTGCGGG 284
Db 61 TTTCACACAGTATGACAGATTCACCTTCCCGCTGAACTCCAGAGCCCTGCGGG 120

QY 285 GAACCTCAGCAACGGTTTCTTCATCAGGACAGATTTGCTGTGGTGGAGAGGGGGTGC 344
Db 121 GAACCTCAGCAACGGTTTCTTCATCAGGACAGATTTGCTGTGGTGGAGAGGGGGTGC 180

QY 345 TCCCTTCCTCCAGACTCGGGTGTCCAGGACAGCGCGCGGGCGGTGCATCTCT 404
Db 181 TCCCTTCCTCCAGACTCGGGTGTCCAGGACAGCGCGCGGGCGGTGCATCTCT 240

QY 405 GACACGCGAGTTGACAAATGACAGCTTCTACGTGGAGATGATCCAGGACAGTACCAGCGC 464
Db 241 GACACGCGAGTTGACAAATGACAGCTTCTACGTGGAGATGATCCAGGACAGTACCAGCGC 300

QY 465 ACAGTGCATATCCCGGCTCTTCTGTCTGGCGAGACGGTACATGATCCGGGCTCT 524
Db 301 ACAGTGCATATCCCGGCTCTTCTGTCTGGCGAGACGGTACATGATCCGGGCTCT 360

QY 525 CTGGAAACAGATGGGCTGCGATGGCCATCATTTCCATCCAGTCAATGTCCACAGATC 584
Db 361 CTGGAAACAGATGGGCTGCGATGGCCATCATTTCCATCCAGTCAATGTCCACAGATC 420

QY 585 CCCACTTTGAGTGTGCTGCAACCGCCCTGGACCTTCTGTGTAGAGAGTTTGTCCACATT 644
Db 421 CCCACTTTGAGTGTGCTGCAACCGCCCTGGACCTTCTGTGTAGAGAGTTTGTCCACATT 480

QY 645 CCAGCCATAGTGACTCTCAGTGTGGAGGGAACCCAGGAAATTTTGTACTTGGAAAT 704
Db 481 CCAGCCATAGTGACTCTCAGTGTGGAGGGAACCCAGGAAATTTTGTACTTGGAAAT 540

QY 705 TGGAGATAGCATCTGGGGACAAGGTGAGCCAGGTAGAGAAAGGGTTTGGCGTTGCTA 764
Db 541 TGGAGATAGCATCTGGGGACAAGGTGAGCCAGGTAGAGAAAGGGTTTGGCGTTGCTA 600

QY 765 GGCTGAAGGGAAGCCACACACTGGCTTCCCTTCCCGAGGGCCCCAACGGGTGTCTCA 824
Db 601 GGCTGAAGGGAAGCCACACACTGGCTTCCCTTCCCGAGGGTCCCAAGGGTGTCTCA 660

QY 825 TGCTACAAAGAGAGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 884
Db 661 TGCTACAAAGAGAGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 885 GAGCTGAAGGAGAGTGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 944
Db 721 GAGCTGAAGGAGAGTGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780

QY 945 CTCCTCTACCCAGGCT-CTCTGACAGTGACCTT 977
Db 781 CTCCTCTACCCAGGCTCTCTGACAGTGACCTT 814

RESULT 6
BUS43314 867 bp mRNA linear EST 13-SEP-2002
LOCUS AGENCOURT_10326796 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6575358
DEFINITION 5', mRNA Sequence.
ACCESSION BUS43314
VERSION BUS43314.1 GI:22853797
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 867)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2772 row: c column: 06
High quality sequence stop: 719.
Location/Qualifiers
1. .867
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6575358"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/notes="Organ: prostate; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

FEATURES
source
1. .867
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6575358"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/notes="Organ: prostate; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 72.9%; Score 800.2; DB 13; Length 867;
Best Local Similarity 99.8%; Pred. No. 1.7e-107;
Matches 840; Conservative 0; Mismatches 8; Indels 5; Gaps 3;

QY 7 CGCGCGCGCGCGCGAGAGAAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 66
Db 1 CGCGCGCGCGCGCGAGAGAAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60

QY 67 CGCGCGCGCGCGCGT 126

Db	596	CTGTGGACCTTTCTGGTAAAGAGATTGTGCCACATTCCAGCCATAAGTACTCTGAGCTGG	655
QY	670	GAAGGGGAAACCCAGGAAATTTCTACTTTGGAAATTTGGAGATAGCATCTGGGACAAGTG	729
Db	656	GAAGGGGAAACCCAGGAAATTTCTACTTTGGAAATTTGGAGATAGCATCTGGGACAAGTG	715
QY	730	GAGCCAGGTA--CAGGAAAGGGTTTGGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCCAC	787
Db	716	GAGCCAGGTACGAGGACACAGGGTTTGGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCAT	775
QY	788	TGGCCCTTCCCTTCCCCAGGGCCCCCAAGGGTGTCATATGC-TACAAAGAGAGCAAGAGA	846
Db	776	TGACCTTCCCTTCCCCAGGTCCCCAAGGGTGTCATATGCTTACAAAGAGCGCAGAAG	835
QY	847	CAGGCCCCAGGGCTTCTGGCTAGAACCCGAA	877
Db	836	ACAGGGCCAGCGCTTTGGGTAGAACCGGAA	866

RESULT 8
BM556790
LOCUS
DEFINITION BM556790 1017 bp mRNA linear EST 20-FEB-2002
5', mRNA sequence.
ACCESSION BM556790
VERSION BM556790.1 GI:18798279
KEYWORDS Est.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NTH-MGC <http://mgc.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
EMAIL: rgs@bbs-rcmail.nih.gov
TISSUE: Tissue Procurement: DCTD/DTF
CDNA LIBRARY: cDNA Library Preparation: Rubin Laboratory
DNA SEQUENCING: DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CLONE DISTRIBUTION: Agencourt Bioscience Corporation
CLONE DISTRIBUTION: MGC clone distribution information can be
FOUND THROUGH: the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
PLATE: LLCMI969 row: k column: 12
High quality sequence stop: 688.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5467523"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 41"
/note="Organ: skin; Vector: pOTB7; Site1: XhoI; Site2:
EcotRI; cDNA made by oligo-dT priming. Directionally cloned
into EcotRI/XhoI sites using the following 5' adaptor:
GGCACCAG(G) . Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN	Query Match	69.7%;	Score 765.4;	DB 12;	Length 1017;
	Best Local Similarity	97.2%;	Pred. No. 1.9e-102;		
	Matches 802;	Conservative	0;	Mismatches 16;	Indels 7;
					Gaps 2

QY	1	CGCAGCCGCGGCGGCGGCGGAGAGAAACCGCGCGCGCGCGCGCGCGCGCGCTGGAGA	60
Db	66	CGCAGCCGCGGCGGCGGCGGAGAGAAACCGCGCGCGCGCGCGCGCGCGCGCTGGAGA	120

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L14M1405 row: b column: 09
 High quality sequence stop: 790.
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4640168"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 20"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 68.3%; Score 750.4; DB 12; Length 790;
 Best Local Similarity 97.7%; Pred. No. 3.3e-100;
 Matches 771; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
 QY 161 GCTGAGTCTGGGACATTCGATATCATCTTCACGCCACCTGCCAAGGACTTTGGTGG 220
 DB 1 GCTGAGTCTGGGACATTCGATATCATCTTCACGCCACCTGCCAAGGACTTTGGTGG 60
 QY 221 TATCTTTTACA CAAGTATGACAGATTCACTTTCCTCCCGTGAACCTCCAGAGGCTG 280
 DB 61 TATCTTTTACA CAAGTATGACAGATTCACTTTCCTCCCGTGAACCTCCAGAGGCTG 120
 QY 281 CGGGGAATCAGACAGGTTCTTCATCAGACACAGATTCTCTGTGGAGAGGGGG 340
 DB 121 CGGGGAATCAGACAGGTTCTTCATCAGACACAGATTCTCTGTGGAGAGGGGG 180
 QY 341 CTGCTCCTTCTCTCCAGACTCGGTGGTTCAGGAGCACGGCGGGCGGGCGGTGATCAT 400
 DB 181 CTGCTCCTTCTCTCCAGACTCGGTGGTTCAGGAGCACGGCGGGCGGGCGGTGATCAT 240
 QY 401 CTCTGACACGAGTTGACATGACAGCTTCTACGTGGAGATGATCCAGGACATACCA 460
 DB 241 CTCTGACACGAGTTGACATGACAGCTTCTACGTGGAGATGATCCAGGACATACCA 300
 QY 461 GGGCAGAGTACATCCCGCCCTCTTCTGTCTGGCGGAGACGGCTACATGATCCGCG 520
 DB 301 GGGCAGAGTACATCCCGCCCTCTTCTGTCTGGCGGAGACGGCTACATGATCCGCG 360
 QY 521 CTCTCTGGAACAGCATGGGTGCGCATGGGCATCATTTTCCATCCAGTCAATGTACAG 580
 DB 361 CTCTCTGGAACAGCATGGGTGCGCATGGGCATCATTTTCCATCCAGTCAATGTACAG 420
 QY 581 CATCCGCCACCTTTGAGCTGCTGCAACCCGCTTGGACCTTCTGTGTAGAGAGTTTGTCCA 640
 DB 421 CATCCGCCACCTTTGAGCTGCTGCAACCCGCTTGGACCTTCTGTGTAGAGAG-TTGTCCA 479
 QY 641 CATTCACGCATTAAGTACTGTGAGCTGGAGGGGAAACCCAGGAATTTTGTACTTGG 700
 DB 480 CATTCACGCATTAAGTACTGTGAGCTGGAGGGGAAACCCAGGAATTTTGTACTTGG 539
 QY 701 AATTTGGAGATAGCATCTGGGACAAAGTGGAGCCAGGTAGAGGAAAGGGTTTGGGGCTT 760
 DB 540 AATCTGGAGATAGCATCTGGGACAAAGTGGAGCCAGGTAGAGGAAAGGGTTTGGGGCTT 599
 QY 761 GCTAGGCTGAAGGGAAGCCACACCATGTGGCTTCCCTTCCCGAGGCCGCCAAGGGTGT 820

Db 600 GCTAGGCTGAAGGGAAGCCACACACTGGGCTTTCCTTCCCGAGNCCCGCCAGAGGGTGT 659
 QY 821 CTATGTCTCAAGAAGAGGCAAGAGACAGGCCCGCCAGGGCTTCTGGCTAGAACCCGAACA 880
 DB 560 CTATGTCTCAAGAAGAGGCAAGAGACAGGCCCGCCAGGGCTTCTGGCTAGAACCCGAACA 719
 QY 881 AAAGGAGCTGAAGGCAAGGCTGGCTGAGAGCATCTGTGACCTGTCTACATCAGCTGGCTC 940
 DB 720 AAAGGAGCTGAAGGCAAGGCTGGCTGAGAGCATCTGTGACCTGTCTACATCAGCTGGCTC 779
 QY 941 CAGCTCTCCC 949
 DB 780 CAGCTCTCCC 788
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 DEFINITION
 mRNA sequence.
 CA489629
 VERSION
 CA489629.1 GI:24952420
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 901)
 NIH-MGC <http://imgc.ncbi.nih.gov/>.
 AUTHORS
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs@mail.nih.gov
 Tissue Procurement: Kristi A. Eglund, Ira Pastan
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L14M1484 row: e column: 19
 High quality sequence stop: 620.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /clone="IMAGE:6722107"
 /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
 HERT-HMEL, LNCaP"
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 /note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
 Subtracted with brain, liver, lung, kidney and muscle.
 Directionally cloned. Priming method: oligo-dT. Average
 insert size: 1800 bp. Library amplification: 26,000 fold.
 Kristi A. Eglund, James J. Vincent, Robert Strausberg,
 Bungkok Lee & Ira Pastan: Discovery of new breast
 cancer genes encoding membrane and secreted proteins.
 Manuscript submitted."

FEATURES

ORIGIN

Query Match 68.3%; Score 749.4; DB 14; Length 901;
 Best Local Similarity 97.3%; Pred. No. 4.3e-100;
 Matches 816; Conservative 0; Mismatches 16; Indels 7; Gaps 5;
 QY 8 GGGGGGGGGCGGAGAGGAAACGGCGCGGGCGGGCGGGCCCTGGAGATGGTCCC 67
 DB 1 GGGGGGGGGCGGAGAGGAAACGGCGCGGGCGGGCGGGCCCTGGAGATGGTCCC 60
 QY 68 CGGGCGGGGGCTGGTGTGTCTGTGCTTCCCGGGTGTCTGGCGGCCACGG 127
 DB 61 CGGGCGGGGGCTGGTGTGTCTGTGCTTCCCGGGTGTCTGGCGGCCACGG 120

Qy	128	CTTCGCTATCCAGTATTATTGTAATTTCAAGTCTGAGTCTGGGACATTCGATACAT	187
Db	121	CTTCGCTATCCAGTATTATTGTAATTTCAAGTCTGAGTCTGGGACATTCGATACAT	180
Qy	188	CTTCACAGCCACACCTCCCAAGACATTTGCTGTATCTTTTCACACAGGTATGAGCAGAT	247
Db	181	CTTCACAGCCACACCTCCCAAGACATTTGCTGTATCTTTTCACACAGGTATGAGCAGAT	240
Qy	248	TCACCTTGTCTCCGCTGAACCTCCAGAGGCTCTCGGGAACTCAGCAACGGTTTCTTCAT	307
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Qy	308	CCAGGACAGATTCCTGTGTGAGAGGGGGCTGTCTTCTCTCCAGACTCGGT	367
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Qy	368	GGTCAGGAGCACGGCGGGCGGTGATCATCTCTGACAAAGCGAGTTGACATACAG	427
Db	361	GGTCAGGAGCACGGCGGGCGGTGATCATCTCTGACAAAGCGAGTTGACATACAG	420
Qy	428	CTTCTAGCTGAGATGATCCAGGACATTCACGCGCACAGCTGACATCCCGCCCTCTT	487
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Qy	488	CCTGCTCGGCGAGACGCTACATGATCCGCGCTCTCTGAAACAGCATGGGTGCCATG	547
Db	481	CCTGCTCGGCGAGACGCTACATGATCCGCGCTCTCTGAAACAGCATGGGTGCCATG	540
Qy	548	GGCCATCATTTCCATCCCACTCAATGTCAACAGATCCCACTTTGAGTGTGCAAC	607
Db	541	GGCCATCATTTCCATCCCACTCAATGTCAACAGATCCCACTTTGAGTGTGCAAC	600
Qy	608	GCCTGACCTTCTGTGAGAGATTTGTCCACATTCACGACATAGTACATCTGAGCT	667
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Qy	725	AAGTGGAGCCAGGTAGAGGAAAGGTTT--GGCGTGTGCTAGCTGAAAGGAGCCAC	782
Db	721	AAGTGGAGCCAGGTAGAGGAAAGGTTTGGCGTTCCTAGCTGAAAGGAGGAAACAC	780
Qy	783	ACCACTGCTCTCCCTTCCCGAGGG--CCCGAAGGTTGCTCATGTACAAGAGAGG	839
Db	781	ACCACTGCTCTCCCTTCCCGAGGGCCCGAAGGCGGCTTCAGGCTACAAGAGAGG	839
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VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 941)			
NIH-MGC http://mgi.nci.nih.gov/.			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: c9apbs-r@mail.nih.gov			
Tissue Procurement: ATCC			
CDNA Library Preparation: Ling Hong/Rubin Laboratory			
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Incyte Genomics, Inc.			
Clone distribution: MGC clone distribution information can be			

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov			
Plate: LCM54 row: m column: 07			
High quality sequence start: 26			
High quality sequence stop: 798.			
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/lab host="DH10B (phage-resistant)"			
/clone lib="NIH MGC 17"			
/note="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;			
Site 2: XhoI; cDNA made by oligo-dT priming.			
Directionally cloned into EcoRI/XhoI sites using the			
following 5' adaptor: GGCACAG(G). Size-selected >500bp			
for average insert size 1.8kb. Library constructed by			
Ling Hong in the laboratory of Gerald M. Rubin (University			
of California, Berkeley) using ZAP-cDNA synthesis kit			
(Stratagene) and Superscript II RT (Life Technologies)."			
ORIGIN			
Query Match			
Best Local Similarity 96.6%; Pred. No. 1.2e-99;			
Matches 805; Conservative 0; Mismatches 23; Indels 5; Gaps 4;			
Qy	193	CAGCCACACCTCCCAAGGACATTTGCTGTATCTTTTCACACAGGTATGACGAGATTCACC	252
Db	829	CAGCCACACCTCCCAAGGACATTTGCTGTATCTTTTCACACAGTA--GACGAGATTCACC	772
Qy	253	TTGTCCCGCTGAACTCCAGAGGCTCTCGGGAACTCAGCAACGGTTTCTTCATCCA-G	311
Db	771	TTGTCCCGCTGAACTCCAGAGGCTCTCGGGAACTCAGCAACGGTTTCTTCATCCA	712
Qy	312	GACGAGATTCCTGGTGGAGAGGGGGCTCTCTCTCCCTCCCAAGACTCGGTGGTC	371
Db	711	GACGAGATTCCTGGTGGAGAGGGGGCTCTCTCTCTCTCCCAAGACTCGGTGGTC	652
Qy	372	CAGGAGACCGGGGGGGGGCTGATCATCTCTGCAACGCGATTTGACAATGACAGCTTC	431
Db	651	CAGGAGACCGGGGGGGGGGGCTGATCATCTCTGCAACGCGATTTGACAATGACAGCTTC	592
Qy	432	TACGTGGAGATGATCCAGGACAGTACCCAGGCGCAGCTGACATCCCGCCCTCTTCCTG	491
Db	591	TACGTGGAGATGATCCAGGACAGTACCCAGGCGCAGCTGACATCCCGCCCTCTTCCTG	532
Qy	492	CTCGGCGGAGCGGCTACATGATCCCGCGCTCTCTGGAACAGCATGGGTGGCATGGGCC	551
Db	531	CTCGGCGGAGCGGCTACATGATCCCGCGCTCTCTGGAACAGCATGGGTGGCATGGGCC	472
Qy	552	ATCATTTCCATCCAGTCAATGTCAACGATTCCTCCACCTTTGAGCTGCTGCAACCGGCC	611
Db	471	ATCATTTCCATCCAGTCAATGTCAACGATTCCTCCACCTTTGAGCTGCTGCAACCG-CC	413
Qy	612	TGGACCTTCTGTTAGAGAGTTTGTCCACATTCAGGCGCATTAAGTGACTCTGAGCTGGGA	671
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Qy	672	AGGGGAAACCCAGGAAATTTTGTACTTGGAAATTTGGAGATAGCATCTGGGGAACAAGTGA	731
Db	352	AGGGGAAACCCAGGAAATTTTGTACTTGGAAATTTGGAGATAGCATCTGGGGAACAAGTGA	293
Qy	732	GCCAGTAGAGAAAGGTTTGGGGTGTCTAGCTGAAAGGGAAGCCACACCACTGGC	791
Db	292	GCCAGTAGAGAAAGGTTTGGGGTGTCTAGCTGAAAGGGAAGCCACACCACTGGC	233
Qy	792	CTTCCCTTCCCGAGGGCCCCCAAGGGTGTCTCATGCTACAAGAGGGAAGGCAAGACAGC	851
Db	232	CTTCCCTTCCCGAGGGCCCCCAAGGGTGTCTCATGCTACAAGAGGGAAGGCAAGACAGC	173
Qy	852	CCAGGGCTTCTGCTAGAACCCGAAACAAAGGAGCTCAAGCGAGGTGGCTGAGAGCC	911

349 TCCTCTCCAGACTCGGGTGTCCAGAGACGCGCGGGGGGTGATCATCTCTGACA 408
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 736 TCCTCTCCAGACTC-GGTGTCCAGAGACGCGCGGGGGGTGATCATCTCTGACA 678
 QY |
 409 ACCAGTTGACATGACAGCTTCTAGTGGAGATGATCCAGACAGTACCCAGCGCACAG 468
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 677 ACCAGTTGACATGACAGCTTCTAGTGGAGATGATCCAGACAGTACCCAGCGCACAG 618
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 529 AACAGATGGGCTGCATGGGCGCATTTCCATCCAGTCAATGATCAGACATCCCA 588
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 589 CTTTTCAGCTGCTGCAACCGCTGACCTTCTGTGAGAGAGTTTGTCCACATCCAG 648
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 497 CTTTTCAGCTGCTGCAACCGCTGACCTTCTGTGAGAGAGTTTGTCCACATCCAG 438
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 649 CCATAAGTGAATCTGAGCTGGGAGGGGAAACCCAGAAATTTTGTCTACTTGGAAATTTGGA 708
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 709 GATAGCATCTGGGACAGTGGAGCGAGCTAGAGGAAGAGTTTGGGCTGTAGGCT 768
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 377 GATAGCATCTGGGACAGTGGAGCGAGCTAGAGGAAGAGTTTGGGCTGTAGGCT 318
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 317 GAAAGGGAAGCCACACCTTCCCTTCCCTTCCAGGCGCCCGGAGGCTGTCTCATGCT 258
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 889 TGAAGGAGGCTGGCTGAGAGGCATCTGTGACCTGTACACTTCACTTGGCTCCAGGCTCC 948
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 197 TGAAGGAGGCTGGCTGAGAGGCATCTGTGACCTGTACACTTGGCTCCAGGCTCC 138
 QY |
 949 CTTACCCAGGCTCTGCAAGTACGCTTCCAGAGGTTTGGAGTGGTTTAAAGAGCT 1008
 Db |
 137 CTTACCCAGGCTCTGCAAGTACGCTTCCAGAGGTTTGGAGTGGTTTAAAGAGCT 78
 QY |
 1009 GGTGTTTGGGACTCAATAAACCTCAGTACTTTTGTAGCAATAAGCTTCTCATCAGG 1068
 Db |
 77 GGTGTTTGGGACTCAATAAACCTCAGTACTTTTGTAGCAATAAGCTTCTCATCAGG 18
 QY |
 1069 TTGCAAAAAA 1085
 Db |
 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 15
 BM674748/c
 LOCUS
 DEFINITION UI-E-EJ0-ahm-e-04-0-UI.s1 UI-E-EJ0 Homo sapiens cDNA clone
 ACCESSION BM674748
 VERSION 1 (bases 1 to 734)
 KEYWORDS Normalization and subtraction: two approaches to facilitate gene
 SOURCE EST. Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS 1. (bases 1 to 734)
 TITLE Normalization and subtraction: two approaches to facilitate gene
 JOURNAL discovery
 MEDLINE Genome Res. 6 (9), 791-806 (1996)
 PUBMED 9704477
 8889548

COMMENT

Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-EJ0-ahm-e-04-0-UI"
 /tissue_type="fetal eyes, lens, eye anterior segment,
 optic nerve, retina, Retina Foveal and Macular, RPE and
 Choroid"
 /dev_stage="fetal and adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-EJ0"
 /notes="Organ: eye; Vector: p77T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-E-EJ0 is a subtracted cDNA library constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into p77T3-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tags for this library are: fetal eyes,
 AGAATCAGA; lens, CGAATAGCA; eye anterior segment,
 AATGCCGAT; optic nerve, CCATTAAGT; retina, CCGGG; Retina
 Foveal and Macular, GTCC; RPE and Choroid, ACTA. This
 library was created for the program, Gene Discovery in the
 Visual System, supported by National Eye Institute (NEI).
 TAG TISSUE=RPE and Choroid
 TAG_LIB=UI-E-EJ0
 TAG_SEQ=ACCTA"

ORIGIN

Query Match 65.1%; Score 715; DB 12; Length 734;
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 Matches 729; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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 Db 734 CTCTCCAGACTC-GGTGTCTCAGAGACGCGCGGGGGGTGATCATCTCTGACAAC 676
 QY 411 GCAGTTGACAATGACAGCTTCTACGTGGAGATGATCCAGACAGTACCCAGCGCACAGCT 470
 Db 675 GCAGTTGACAATGACAGCTTCTACGTGGAGATGATCCAGACAGTACCCAGCGCACAGCT 616
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 Db 615 GACATCCCGGCTCTCTCTGCTCGCGAGAGCGGTACATGATCCGCGCTCTCTGGAA 556
 QY 531 CAGCATGGGCTGCCATGGGCCATCATTTCCATCCAGTCAATGTCCAGACATCCCCACC 590
 Db 555 CAGCATGGGCTGCCATGGGCCATCATTTCCATCCAGTCAATGTCCAGACATCCCCACC 496
 QY 591 TTTGAGCTGCTGCAACCGGCTGGACCTTCTGTAGAGAGTTGTCCACATCCAGCC 650
 Db 495 TTTGAGCTGCTGCAACCGGCTGGACCTTCTGTAGAGAGTTGTCCACATCCAGCC 436

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QY	711	TAGCATCTGGGGACAAGTGGAGCAGGTAGAGGAAAGGGTTTGGCGCTTGTCTAGGCTGA	770
Db	375	TAGCATCTGGGGACAAGTGGAGCAGGTAGAGGAAAGGGTTTGGCGCTTGTCTAGGCTGA	316
QY	771	AAGGAGCCACACCACTGGCTTCCCTTCCCAGGGSCCCCAAGGGTGTCTCATGCTAC	830
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QY	831	AAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAAAGGAGCTG	890
Db	255	AAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAAAGGAGCTG	196
QY	891	AAGCAGGTGGCTTGAGAGCCATCTGTGACTGTGCACACTCACTGGCTCCAGCCTCCCC	950
Db	195	AAGCAGGTGGCTTGAGAGCCATCTGTGACTGTGCACACTCACTGGCTCCAGCCTCCCC	136
QY	951	TACCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGGAGTGGTTTAAAGAGCTGG	1010
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QY	1011	TGTTGGGGACTCAATAAACCTCACTGACTTTTTCAGCAATAAGCTTCTCATCAGGGTT	1070
Db	75	TGTTGGGGACTCAATAAACCTCACTGACTTTTTCAGCAATAAGCTTCTCATCAGGAAA	16
QY	1071	GCAAAAAAAAAAAAAA	1085
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